

OS Human endogenous retrovirus.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 15, 2005, 23:53:58 ; Search time 31202 Seconds
(without alignments)
11774.484 Million cell updates/sec

Title: US-10-717-580-11
Perfect score: 7582
Sequence: 1 caacaatcggtataaacc.....tattaaatcttgcacrtgcr 7582

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7489.6	98.8	7582	6	BD196245
2	7489.6	98.8	7582	6	BD267487
3	7489.6	98.8	7582	6	AX000966
4	7489.6	98.8	7582	6	AX027480
5	6448	85.0	10222	9	AY101582
6	6448	85.0	10222	9	AY101585
7	6448	85.0	56093	6	AX329572
8	6448	85.0	56093	9	HSAC000064
9	6448	85.0	149194	9	AC007566
10	6446.4	85.0	10222	9	AY101583
11	6440	84.9	10222	9	AY101584
12	6436	84.9	10499	6	BD221808
13	6436	84.9	10499	6	AX007980
14	6346.4	83.7	10229	9	AY101586
15	6344.8	83.7	10229	9	AY101587
16	6344.8	83.7	184575	9	AC145964
17	6269.6	82.7	10230	9	AY101588
18	6269.6	82.7	10230	9	AY101589
19	6037.8	79.6	10122	9	AY101590

20	5025.8	79.5	10124	9	AY101591	AY101591 Pongo pyg
21	5956.8	78.6	10246	9	AY101593	AY101593 Hylobates
22	5950.4	78.5	10248	9	AY101592	AY101592 Hylobates
23	5824.2	76.8	158033	9	AC018926	AC018926 Homo sapi
24	5492	72.4	105989	9	AC008121	AC008121 Homo sapi
25	5492	72.4	110000	2	AC009727_2	Continuation (3 of
26	4755.6	62.7	117321	2	AC092510	AC092510 Papio anu
27	4302.2	56.7	114621	9	AC005187	AC005187 Homo sapi
28	4295.8	56.7	46575	2	AC080036	AC080036 Homo sapi
29	4162	54.9	111140	9	AL592310	AL592310 Human DNA
30	3944.6	52.0	183680	9	AC098859	AC098859 Homo sapi
31	3779.8	49.9	73070	9	AL590143	AL590143 Human DNA
32	3731.6	49.2	173788	9	AC022555	AC022555 Homo sapi
33	3731.6	49.2	186540	9	AC090341	AC090341 Homo sapi
34	3731.6	49.2	187837	9	AC079065	AC079065 Homo sapi
35	3716.6	49.0	160883	2	AL158814	AL158814 Homo sapi
36	3537.2	46.7	137947	9	HS4514	AL023581 Human DNA
37	3442.8	45.4	153444	2	AC040948	AC040948 Homo sapi
38	3442.8	45.4	205035	9	CNS00008	AL049870 Human Chr
39	3438.2	45.3	101846	9	HS19711	AL031390 Human DNA
40	3438.2	45.3	224629	2	AC139260	AC139260 Homo sapi
41	3420.6	45.1	68693	9	AC108746	AC108746 Homo sapi
42	3367.4	44.4	118112	9	AC055713	AC055713 Homo sapi
43	3367.4	44.4	197549	2	AC145423	AC145423 Homo sapi
44	3300.6	43.5	169250	9	AP002812	AP002812 Homo sapi
45	3290.2	43.4	134412	2	AP002377	AP002377 Homo sapi

ALIGNMENTS

BD196245 7582 bp DNA linear PAT 17-JUL-2003
Endogenous retroviral sequences, associated with autoimmune diseases and/or with pregnancy disorders.

BD196245
BD196245.1 GI:33006015
JP 2002512530-A/11.
unidentified
unclassified.

REFERENCE 1 (bases 1 to 7582)

AUTHORS Beseme,F., Blond,J.L., Bouton,O., Mandrand,B. and Mallet,F.

TITLE Endogenous retroviral sequences, associated with autoimmune diseases and/or with pregnancy disorders

JOURNAL Patent: JP 2002512530-A 11 23-APR-2002;

COMMENT BIO MERIEUX

OS Unidentified

PN JP 2002512530-A/11

PD 23-APR-2002

PF 06-JUL-1998 JP 1999508244

PR 07-JUL-1997 FR 97/08815

PI FREDERIC BESEME,JEAN LUC BLOND,OLIVIER BOUTON,BERNARD MANDRAND,

PI FRANCOIS MALLET

PC C12N15/48,C07K14/15,C12Q/68,C07K16/10,G01N33/569 CC

Strandedness: Single;

CC Topology: Linear;

CC Endogenous retroviral sequences, associated with autoimmune diseases

CC and/or with pregnancy disorders

PH Key Location/Qualifiers

FT source 1..7582

Location/Qualifiers

1..7582

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 98.8%; Score 7489.6; DB 6; Length 7582;

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2005, 22:59:08 ; Search time 21789 Seconds
(without alignments)
13245.366 Million cell updates/sec

Title: US-10-717-580-11

Perfect score: 7582

Sequence: 1 caacaatcggtataaacc.....tattaaatcttgacrtgcr 7582

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180.4	28.8	2748	3	CR605851 full-leng
2	2176.4	28.7	2749	3	CR617248 full-leng
3	2174.4	28.7	2500	3	CR622175 full-leng
4	2169.4	28.6	2748	3	CR625046 full-leng
5	2147.4	28.3	2716	3	CR613169 full-leng
6	969	12.8	1071	5	CR635066 full-leng
7	921.2	12.1	998	5	CR637769 full-leng
8	909.6	12.0	1058	5	CR6378303 full-leng
9	908.6	12.0	935	5	CR6391741 full-leng
10	885.2	11.7	955	5	CR6347952 full-leng
11	885	11.7	1019	5	CR6347952 full-leng
12	866.6	11.4	1014	5	CR6347952 full-leng
13	848.8	11.2	6400	3	CR6378304 full-leng
14	834.8	11.0	924	5	CR6347314 full-leng
15	820.8	10.8	931	5	CR6389656 full-leng
16	820	10.8	903	5	CR6389656 full-leng
17	812	10.7	872	5	CR6389656 full-leng
18	804	10.6	883	5	CR6389656 full-leng
19	803.8	10.6	966	5	CR6389656 full-leng
20	789.2	10.4	877	5	CR6347619 full-leng
21	776.2	10.2	921	5	CR6347619 full-leng
22	771	10.2	836	5	CR6389656 full-leng
23	768.6	10.1	995	5	CR6389657 full-leng
24	765.4	10.1	844	5	CR6347111 full-leng

25	764.8	10.1	828	5	CR6367907	CR6367907
26	753.8	9.9	846	5	CR6368078	CR6368078
27	751.6	9.9	900	5	CR6459153	CR6459153
28	724.6	9.6	758	5	CR6357208	CR6357208
29	723.4	9.5	879	5	CR6325902	CR6325902
30	719.4	9.5	924	5	CR6403328	CR6403328
31	709.4	9.4	771	4	CR6087886	CR6087886
32	697.2	9.2	723	1	CR6138405	CR6138405
33	677.4	8.9	702	1	CR6138097	CR6138097
34	673.6	8.9	795	8	CR6119889	CR6119889
35	665.6	8.8	714	2	CR6734284	CR6734284
36	665	8.8	719	7	CR6272394	CR6272394
37	649.8	8.6	944	5	CR6368759	CR6368759
38	639.6	8.4	744	8	CR62601435	CR62601435
39	637.8	8.4	833	8	CR6207553	CR6207553
40	621.6	8.2	658	5	CR6430050	CR6430050
41	621.6	8.2	851	7	CR675248	CR675248
42	617	8.1	776	8	CR6351025	CR6351025
43	616.2	8.1	738	9	CR6408776	CR6408776
44	615.2	8.1	733	5	CR6374329	CR6374329
45	612	8.1	792	5	CR6409304	CR6409304

ALIGNMENTS

RESULT 1	CR605851	2748 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CSODE012YJ24 of Placenta of Homo sapiens				
DEFINITION	CR605851				
ACCESSION	CR605851				
VERSION	CR605851.1	GI:50486658			
KEYWORDS	HTC; CNSLT cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2748)				
AUTHORS	Li, W.B., Gruber, C., Jesses, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 2748)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr				
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1..2748				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="CSODE012YJ24"				
	/tissue_type="Placenta"				
	/plasmid="pCMVSPORT_6"				

ORIGIN	Query Match	28.8%	Score 2180.4	DB 3	Length 2748
	Best Local Similarity	98.4%	Pred. No. 0		
	Matches 2171	Conservative 34	Mismatches 0	Indels 1	Gaps 1
Qy	5352	GATACATCTCGGAGGACCTACCCAGTCATTTATYATCCCACTGGGTTAAAGTG	5411		
Db	544	GATACATCTCGGAGGACCTACCCAGTCATTTATCTATCTACCCCACTGGGTTAAAGTG	603		